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SEQUENCE LISTING TECH CENTER 1600/2900 MAR 21 2002

TECH CENTER 1600/2900

<110> Lechler, Robert I.  
Dorling, Anthony

<120> IMMUNOSUPPRESSION BY BLOCKING T CELL CO-STIMULATION SIGNAL 2 (B7/CD28  
INTERACTION)

<130> 2292/0H795

<140> US 09/674,462

<141> 2001-05-08

<150> PCT/ GB99/01350

<151> 1999-04-30

<160> 27

<170> PatentIn Ver. 2.1

<210> 1

<211> 223

<212> PRT

<213> Sus scrofa

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Ser Arg Thr Trp Pro Cys Thr Ala Leu Phe Ser Leu Leu Phe Ile Pro  
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Val Phe Ser Lys Gly Met His Val Ala Gln Pro Ala Val Val Leu Ala  
35 40 45

Asn Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser Ala Gly  
50 55 60

Lys Ala Ala Glu Val Arg Val Thr Val Leu Arg Arg Ala Gly Ser Gln  
65 70 75 80

Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asp Glu Leu Thr  
85 90 95

Phe Leu Asp Asp Ser Thr Cys Thr Gly Thr Ser Thr Glu Asn Lys Val  
100 105 110

Asn Leu Thr Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile  
115 120 125

Cys Lys Val Glu Leu Leu Tyr Pro Pro Pro Tyr Tyr Val Gly Met Gly  
130 135 140

Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser  
145 150 155 160

Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe  
165 170 175

Tyr Ser Phe Leu Ile Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys  
180 185 190

Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu  
195 200 205

Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn  
210 215 220

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gccccaaacctg cagtagtgct ggccaaacagc cgggggttgc ccagcttgc gtgtgagttat 180  
gggtctgcag gcaaagctgc cgaggtccgg gtgacagtgc tgcggcgggc cggcagccag 240  
atgactgaag tctgtgccgc gacatatact gtggaggatg agttgacctt ctttgcgtac 300  
tctacatgca ctggcaccc caccgaaaac aaagtgaacc tcaccatcca agggctgaga 360  
gccgtggaca ctgggctcta catctgcaag gtggagctcc tgttacccacc accctactat 420  
gtgggtatgg gcaacgggac ccagattat gtcatgtatc cagaaccatg cccagattct 480  
gatttcctgc tctggatcct ggcagcgtt agttcagggt tttttttta cagcttcctc 540  
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<211> 400  
<212> PRT  
<213> Artificial Sequence

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<223> pCTLA4-Ig construct (Figure 4)

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			20					25					30		
Val	Phe	Ser	Lys	Gly	Met	His	Val	Ala	Gln	Pro	Ala	Vál	Val	Leu	Ala
			35				40					45			
Asn	Ser	Arg	Gly	Val	Ala	Ser	Phe	Val	Cys	Glu	Tyr	Gly	Ser	Ala	Gly
						55					60				
Lys	Ala	Ala	Glu	Val	Arg	Val	Thr	Val	Leu	Arg	Arg	Ala	Gly	Ser	Gln
					65		70			75					80
Met	Thr	Glu	Val	Cys	Ala	Ala	Thr	Tyr	Thr	Val	Glu	Asp	Glu	Leu	Thr
					85			90						95	
Phe	Leu	Asp	Asp	Ser	Thr	Cys	Thr	Gly	Thr	Ser	Thr	Glu	Asn	Lys	Val
					100			105					110		
Asn	Leu	Thr	Ile	Gln	Gly	Leu	Arg	Ala	Val	Asp	Thr	Gly	Leu	Tyr	Ile
					115		120					125			
Cys	Lys	Val	Glu	Leu	Leu	Tyr	Pro	Pro	Pro	Tyr	Tyr	Val	Gly	Met	Gly
					130		135					140			
Asn	Gly	Thr	Gln	Ile	Tyr	Val	Ile	Asp	Pro	Glu	Pro	Cys	Pro	Asp	Ser
					145		150			155					160
Asp	Gly	Gly	Ser	Gly	Gly	Ala	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr
					165			170					175		
His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser
					180			185					190		
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
						195		200				205			
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro
					210		215				220				
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
						225		230			235				240
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val
					245			250					255		
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
					260			265					270		
Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr
					275			280				285			

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
290 295 300

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys  
305 310 315 320

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser  
325 330 335

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp  
340 345 350

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser  
355 360 365

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala  
370 375 380

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
385 390 395 400

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<212> DNA  
<213> Phage library

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ctccagggaa ggggctggag tgggtctca g tattcgtgg tagtgggtgtt agcacatact 180  
acgcagactc cgtgaaggcc cggttacca tctccagaga caattccaag aacacgctgt 240  
atctgcaa at gaacagccctg agagccgagg acacggccgt gtattactgt gcaagagctg 300  
gtcgtat tttt gtttactat tggggccaag gtaccctggt caccgtctcg agtgggtggag 360  
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cctcagcgtc tgggaccccc ggcagcggg tcaccatctc ttgttcttgg a agcagctcca 480  
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tcatctatag gaataatcag cggccctcag gggcccttca ccgattcttctt ggctccaat 600  
ctggcacctc agcctccctt gccatcagtg ggctccggc cggaggatgag gctgattatt 660  
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gt 722

<210> 5  
<211> 240  
<212> PRT  
<213> Phage library

<400> 5

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Ala Gly Arg Ile Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
100 105 110

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly  
115 120 125

Gly Ser Ala Leu Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly  
130 135 140

Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn  
145 150 155 160

Ile Gly Ser Asn Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala  
165 170 175

Pro Lys Leu Leu Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro  
180 185 190

Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile  
195 200 205

Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp  
210 215 220

Asp Asp Ser Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
225 230 235 240

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<210> 7  
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	ccggcagccc	ccagggaaagg	gactggagtg	gattgggtat	atctattaca	gtgggagcac	180
	caactacaac	ccctccctca	agagtcgagt	caccatataca	gtagacacgt	ccaagaacca	240
	gttctccctg	aagctgagct	ctgtgaccgc	tgcggacacg	gccgtgtatt	actgtgcaag	300
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	tggaggcgg	tcaggcggag	gtggctctgg	cgttagtgca	cttcagtctg	tgctgactca	420
	gccaccctca	gcgtctggga	ccccccggca	gagggtcacc	atctcttgtt	ctggaagcag	480
	ctccaacatc	ggaagtaatt	atgtatactg	gtaccagcag	ctcccaggaa	cggcccccaa	540
	actcctcatc	tataggaata	atcagcggcc	ctcaggggtc	cctgaccgat	tctctggctc	600
	caagtctggc	acctcagcct	ccctggccat	cagtgggctc	cggtccgagg	atgaggctga	660
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	cgtccttaqqt	qcqqccqc					738

<210> 8  
<211> 739  
<212> DNA  
<213> Phage library

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caggcccctg gacaagggtc ttagtggatg ggaataatca accctaqtgg tggtaqcaca 180

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caagctacgc acagaagttc cagggcagag tcaccatgac cagggacacg tccacgagca 240
cagtctacat ggagctgagc agcctgagat ctgaggacac ggcctgttat tactgtgcaa 300
gaatggctcc ctatgtgaat acgcttggtt tttggggcca agtaccctg gtcaccgtct 360
cgagtggtgg aggccgttca ggcggaggtg gctctggcg tagtgacatt cagtctgtgc 420
tgactcagga ccctgctgtg tctgtggct tggcacagac agtcaggatc acatgccaag 480
taggagacag cctcagaagc tattatgcaa gctggtacca gcagaagcca ggacaggccc 540
ctgtacttgt catctatggt aaaaacaacc ggccttcagg gatcccagac cgattctctg 600
gctccagctc aggaaacaca gtttccttga ccatcactgg ggctcaggcg gaagatgagg 660
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<210> 9  
<211> 729  
<212> DNA  
<213> Phage library

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gccagatgcc cgggaaaggc ctggagtgga tggggatcat ctatcctgt gactctgata 180
ccagatacag cccgtccttc caaggccagg tcaccatctc agccgacaag tccatcagca 240
ccgcctacct gcagtggagc agcctgaagg cctcggacac gcccgtgtat tactgtgcaa 300
gattttcgct tggtgtttt gactattggg gccaaggta cctggtcacc gtctcgagtg 360
gtggaggcgg ttcaggcgg a ggtggctctg gcggttagtgc acttgacatc cagttgaccc 420
agtctccatg ttccctgtctg catctgttagg agacagagtc accatcaatt gccgggcccag 480
tcagggcatt agcagttatt tagcctggta tcagaaaaa ccagggaaag cccctaagct 540
cctggcttat gctgcattcca ctttgcaaaag tggggtccca tcaaggttca gcggcagtgg 600
atctggaca gaattcactc tcacaatcag cagcctgcag cctgaagatt ttgcaactta 660
ttactgtcaa cagcttaata gttaccgctt gacgttcgcc caagggacca agctggaaat 720
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<210> 10  
<211> 240  
<212> PRT  
<213> Phage library

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20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

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65	70	75	80
Leu Gln Met Asn Ser	Leu Arg Ala Glu Asp	Thr Ala Val Tyr Tyr	Cys
85	90	95	
Ala Arg Ala Gly Arg Ile Leu Phe Asp	Tyr Trp Gly Gln Gly	Thr Leu	
100	105	110	
Val Thr Val Ser Ser Gly Gly	Gly Ser Gly Gly	Gly Ser Gly	
115	120	125	
Gly Ser Ala Leu Gln Ser Val	Leu Thr Gln Pro Pro	Ser Ala Ser Gly	
130	135	140	
Thr Pro Gly Gln Arg Val Thr Ile Ser Cys	Ser Gly Ser Ser Ser	Asn	
145	150	155	160
Ile Gly Ser Asn Tyr Val Tyr Trp Tyr	Gln Gln Leu Pro Gly	Thr Ala	
165	170	175	
Pro Lys Leu Leu Ile Tyr Arg Asn Asn	Gln Arg Pro Ser Gly	Val Pro	
180	185	190	
Asp Arg Phe Ser Gly Ser Lys	Ser Gly Thr Ser Ala	Ser Leu Ala Ile	
195	200	205	
Ser Gly Leu Arg Ser Glu Asp	Glu Ala Ser Tyr Tyr	Cys Ala Ala Trp	
210	215	220	
Asp Asp Ser Leu Val Phe	Gly Gly Thr Lys	Leu Thr Val Leu Gly	
225	230	235	240

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 <211> 246  
 <212> PRT  
 <213> Phage library

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 20 25 30

Ser Gly Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly  
 35 40 45

Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn  
50 55 60

Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Met Arg Lys Asp Lys Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly  
115 120 125

Gly Ser Gly Gly Ser Ala Leu Gln Ser Val Leu Thr Gln Pro Pro Ser  
130 135 140

Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser  
145 150 155 160

Ser Ser Asn Ile Gly Ser Asn Tyr Val Tyr Trp Tyr Gln Gln Leu Pro  
165 170 175

Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Asn Asn Gln Arg Pro Ser  
180 185 190

Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser  
195 200 205

Leu Ala Ile Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Val  
210 215 220

Ala Ala Trp Asp Asp Ser Leu Phe Val Phe Gly Gly Thr Lys Leu  
225 230 235 240

Thr Val Leu Gly Ala Ala  
245

<210> 12  
<211> 242  
<212> PRT  
<213> Phage library

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 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Léu Glu Trp Met  
 35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe  
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr  
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Arg Val Ala Pro Tyr Val Asn Thr Leu Val Phe Trp Gly Gln Gly  
 100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly  
 115 120 125

Ser Gly Gly Ser Ala Leu Ser Ser Glu Leu Thr Gln Asp Pro Ala Val  
 130 135 140

Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser  
 145 150 155 160

Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala  
 165 170 175

Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro  
 180 185 190

Asp Arg Phe Ser Gly Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile  
 195 200 205

Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg  
 210 215 220

Asp Ser Ser Gly Phe Thr Val Phe Gly Gly Thr Lys Leu Thr Val  
 225 230 235 240

Leu Gly

<210> 13  
 <211> 240  
 <212> PRT  
 <213> Phage library

<400> 13

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20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Phe Ser Leu Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
100 105 110

Val Thr Val Ser Ser Gly Gly Ser Gly Gly Gly Ser Gly  
115 120 125

Gly Ser Ala Leu Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser  
130 135 140

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly  
145 150 155 160

Ile Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro  
165 170 175

Lys Leu Leu Val Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser  
180 185 190

Arg Phe Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser  
195 200 205

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn  
210 215 220

Ser Tyr Arg Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg  
225 230 235 240

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cctggccctg cactctcctg tttttcttc tcttcatccc tgtcttctgc aaagcaatgc 180  
acgtggccca gcctgctgtg gtactggcca gcagccgagg catgccagc tttgtgtgtg 240  
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gccaggtgac tgaagtctgt gcccgaacct acatgatggg gaatgagttg accttcctag 360  
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<212> PRT  
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20 25 30  
  
Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala  
35 40 45  
  
Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly  
50 55 60  
  
Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln  
65 70 75 80  
  
Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr  
85 90 95  
  
Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val  
100 105 110  
  
Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile  
115 120 125

Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly  
 130 135 140

Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser  
 145 150 155 160

Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe  
 165 170 175

Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys  
 180 185 190

Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu  
 195 200 205

Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn  
 210 215 220

<210> 16

<211> 773

<212> DNA

<213> Homo sapiens

<400> 16

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 ctggatcgga cctggAACCT gggcgagaca gtggagctga agtgcgcagg gctgctgtcc 180  
 aacccgacgt cgggctgctc gtggctcttc cagccgcgcg gcccgcgcg cagtcccacc 240  
 ttcctccat acctctccca aaacaagccc aaggcgccg aggggcttggc caccaggcg 300  
 ttctcgggca agaggttggg ggacaccttc gtctcaccctc tgagcgactt ccgcggagag 360  
 aacgagggtct actatttctg ctcggccctg agcaactccaa tcatgtactt cagccacttc 420  
 gtgccggtct tcctgcccagc gaagcccacc acgacgcccag cccgcgacc accaacaccg 480  
 gcccacca tcgcgtcgca gcccctgtcc ctgcgcggcagg aggcgtgccg gccagcggcg 540  
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<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 17

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<220>  
<223> PCR primer

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